

e

26

gat ttt gca gga gac ggg tta ttt aca agc tgg acg cat gaa aaa aat	288
Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn	
80 85 90 95	
tggtgg aaa aaagcg cat aat atc tta ctt cca agc ttc agt cag cag gca	336
Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala	
100 105 110	
atg aaa ggc tat cat gcgatg atg gtc gat atc gcc gtg cag ctt gtt	384
Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val	
115 120 125	
caa aag tgg gag cgt cta aat gca gat gag cat att gaa gta ccg gaa	432
Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu	
130 135 140	
gac atg aca cgt tta acg ctt gat aca att ggt ctt tgc ggc ttt aac	480
Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn	
145 150 155	
tat cgc ttt aac agc ttt tac cga gat cag cct cat cca ttt att aca	528
Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr	
160 165 170 175	
agt atg gtc cgt gca ctg gat gaa gca atg aac aag ctg cag cga gca	576
Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala	
180 185 190	
aat cca gac gac cca gct tat gat gaa aac aag cgc cag ttt caa gaa	624
Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu	
195 200 205	
gat atc aag gtg atg aac gac cta gta gat aaa att att gca gat cgc	672
Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg	
210 215 220	
aaa gca agc ggt gaa caa agc gat gat tta tta acg cat atg cta aac	720
Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn	
225 230 235	
gga aaa gat cca gaa acg ggt gag ccg ctt gat gac gag aac att cgc	768
Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg	
240 245 250 255	
tat caa att att aca ttc tta att gcggga cac gaa aca aca agt ggt	816
Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly	
260 265 270	
ctt tta tca ttt gcg ctg tat ttc tta gtg aaa aat cca cat gta tta	864
Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu	
275 280 285	

27

caa aaa gca gca gaa gaa gca gca cga gtt cta gta gat cct gtt cca	912
Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro	
290 295 300	
agc tac aaa caa gtc aaa cag ctt aaa tat gtc ggc atg gtc tta aac	960
Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn	
305 310 315	
gaa gcg ctg cgc tta tgg cca act gct cct gcg ttt tcc cta tat gca	1008
Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala	
320 325 330 335	
aaa gaa gat acg gtg ctt gga gga gaa tat cct tta gaa aaa ggc gac	1056
Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp	
340 345 350	
gaa cta atg gtt ctg att cct cag ctt cac cgt gat aaa aca att tgg	1104
Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp	
355 360 365	
gga gac gat gtg gaa gag ttc cgt cca gag cgt ttt gaa aat cca agt	1152
Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser	
370 375 380	
gcg att ccg cag cat gcg ttt aaa ccg ttt gga aac ggt cag cgt gcg	1200
Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala	
385 390 395	
tgt atc ggt cag cag ttc gct ctt cat gaa gca acg ctg gta ctt ggt	1248
Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly	
400 405 410 415	
atg atg cta aaa cac ttt gac ttt gaa gat cat aca aac tac gag ctg	1296
Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu	
420 425 430	
gat att aaa gaa act tta acg tta aaa cct gaa ggc ttt gtg gta aaa	1344
Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys	
435 440 445	
gca aaa tcg aaa aaa att ccg ctt ggc ggt att cct tca cct agc act	1392
Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr	
450 455 460	
gaa cag tct gct aaa aaa gta cgc aaa aag gca gaa aac gct cat aat	1440
Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn	
465 470 475	
acg ccg ctg ctt gtg cta tac ggt tca aat atg gga aca gct gaa gga	1488
Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly	
480 485 490 495	

28

acg gcg cgt gat tta gca gat att gca atg agc aaa gga ttt gca ccg	1536
Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro	
500 505 510	
cag gtc gca acg ctt gat tca cac gcc gga aat ctt ccg cgc gaa gga	1584
Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly	
515 520 525	
gct gta tta att gta acg gcg tct tat aac ggt cat ccg cct gat aac	1632
Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn	
530 535 540	
gca aag caa ttt gtc gac tgg tta gac caa gcg tct gct gat gaa gta	1680
Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val	
545 550 555	
aaa ggc gtt cgc tac tcc gta ttt gga tgc gcc gat aaa aac tgg gct	1728
Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala	
560 565 570 575	
act acg tat caa aaa gtg cct gct ttt atc gat gaa acg ctt gcc gct	1776
Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala	
580 585 590	
aaa ggg gca gaa aac atc gct gac cgc ggt gaa gca gat gca agc gac	1824
Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp	
595 600 605	
gac ttt gaa ggc aca tat gaa gaa tgg cgt gaa cat atg tgg agt gac	1872
Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp	
610 615 620	
gta gca gcc tac ttt aac ctc gac att gaa aac agt gaa gat aat aaa	1920
Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys	
625 630 635	
tct act ctt tca ctt caa ttt gtc gac agc gcc gcg gat atg ccg ctt	1968
Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu	
640 645 650 655	
gcg aaa atg cac ggt gcg ttt tca acg aac gtc gta gca agc aaa gaa	2016
Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu	
660 665 670	
ctt caa cag cca ggc agt gca cga agc acg cga cat ctt gaa att gaa	2064
Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu	
675 680 685	
ctt cca aaa gaa gct tct tat caa gaa gga gat cat tta ggt gtt att	2112
Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile	
690 695 700	

29

cct cgc aac tat gaa gga ata gta aac cgt gta aca gca agg ttc ggc	2160
Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly	
705 710 715	
cta gat gca tca cag caa atc cgt ctg gaa gca gaa gaa gaa aaa tta	2208
Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu	
720 725 730 735	
gct cat ttg cca ctc gct aaa aca gta tcc gta gaa gag ctt ctg caa	2256
Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln	
740 745 750	
tac gtg gag ctt caa gat cct gtt acg cgc acg cag ctt cgc gca atg	2304
Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met	
755 760 765	
gct gct aaa acg gtc tgc ccg ccg cat aaa gta gag ctt gaa gcc ttg	2352
Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu	
770 775 780	
ctt gaa aag caa gcc tac aaa gaa caa gtg ctg gca aaa cgt tta aca	2400
Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr	
785 790 795	
atg ctt gaa ctg ctt gaa aaa tac ccg gcg tgt gaa atg aaa ttc agc	2448
Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser	
800 805 810 815	
gaa ttt atc gcc ctt ctg cca agc ata cgc ccg cgc tat tac tcg att	2496
Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile	
820 825 830	
tct tca tca cct cgt gtc gat gaa aaa caa gca agc atc acg gtc agc	2544
Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser	
835 840 845	
gtt gtc tca gga gaa gcg tgg agc gga tat gga gaa tat aaa gga att	2592
Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile	
850 855 860	
gcg tcg aac tat ctt gcc gag ctg caa gaa gga gat acg att acg tgc	2640
Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys	
865 870 875	
ttt att tcc aca ccg cag tca gaa ttt acg ctg cca aaa gac cct gaa	2688
Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu	
880 885 890 895	
acg ccg ctt atc atg gtc gga ccg gga aca ggc gtc gcg ccg ttt aga	2736
Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg	
900 905 910	

30

ggc ttt gtg cag gcg cgc aaa cag cta aaa gaa caa gga cag tca ctt 2784
 Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu
 915 920 925

gga gaa gca cat tta tac ttc ggc tgc cgt tca cct cat gaa gac tat 2832
 Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr
 930 935 940

ctg tat caa gaa gag ctt gaa aac gcc caa agc gaa ggc atc att acg 2880
 Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr
 945 950 955

ctt cat acc gct ttt tct cgc atg cca aat cag ccg aaa aca tac gtt 2928
 Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val
 960 965 970 975

cag cac gta atg gaa caa gac ggc aag aaa ttg att gaa ctt ctt gat 2976
 Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp
 980 985 990

caa gga gcg cac ttc tat att tgc gga gac gga agc caa atg gca cct 3024
 Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro
 995 1000 1005

gcc gtt gaa gca acg ctt atg aaa agc tat gct gac gtt cac caa gtg 3072
 Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val
 1010 1015 1020

agt gaa gca gac gct cgc tta tgg ctg cag cag cta gaa gaa aaa ggc 3120
 Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly
 1025 1030 1035

cga tac gca aaa gac gtg tgg gct ggg taa 3150
 Arg Tyr Ala Lys Asp Val Trp Ala Gly
 1040 1045

<210> 2

<211> 1048

<212> PRT

<213> Bacillus megaterium

<400> 2

Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys Asn
 1 5 10 15

Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile
 20 25 30

Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val
 35 40 45

31

Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu
 50 55 60

Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp
 65 70 75 80

Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn Trp
 85 90 95

Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
 100 105 110

Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln
 115 120 125

Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp
 130 135 140

Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr
 145 150 155 160

Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser
 165 170 175

Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn
 180 185 190

Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp
 195 200 205

Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys
 210 215 220

Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly
 225 230 235 240

Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr
 245 250 255

Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu
 260 265 270

Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln
 275 280 285

Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser
 290 295 300

Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu
 305 310 315 320

32

Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys
 325 330 335

Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu
 340 345 350

Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly
 355 360 365

Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala
 370 375 380

Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys
 385 390 395 400

Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met
 405 410 415

Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp
 420 425 430

Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala
 435 440 445

Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu
 450 455 460

Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn Thr
 465 470 475 480

Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly Thr
 485 490 495

Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro Gln
 500 505 510

Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala
 515 520 525

Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn Ala
 530 535 540

Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys
 545 550 555 560

Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala Thr
 565 570 575

Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala Lys
 580 585 590

33

Gly	Ala	Glu	Asn	Ile	Ala	Asp	Arg	Gly	Glu	Ala	Asp	Ala	Ser	Asp	Asp	595	600	605	
Phe	Glu	Gly	Thr	Tyr	Glu	Glu	Trp	Arg	Glu	His	Met	Trp	Ser	Asp	Val	610	615	620	
Ala	Ala	Tyr	Phe	Asn	Leu	Asp	Ile	Glu	Asn	Ser	Glu	Asp	Asn	Lys	Ser	625	630	635	640
Thr	Leu	Ser	Leu	Gln	Phe	Val	Asp	Ser	Ala	Ala	Asp	Met	Pro	Leu	Ala	645	650	655	
Lys	Met	His	Gly	Ala	Phe	Ser	Thr	Asn	Val	Val	Ala	Ser	Lys	Glu	Leu	660	665	670	
Gln	Gln	Pro	Gly	Ser	Ala	Arg	Ser	Thr	Arg	His	Leu	Glu	Ile	Glu	Leu	675	680	685	
Pro	Lys	Glu	Ala	Ser	Tyr	Gln	Glu	Gly	Asp	His	Leu	Gly	Val	Ile	Pro	690	695	700	
Arg	Asn	Tyr	Glu	Gly	Ile	Val	Asn	Arg	Val	Thr	Ala	Arg	Phe	Gly	Leu	705	710	715	720
Asp	Ala	Ser	Gln	Gln	Ile	Arg	Leu	Glu	Ala	Glu	Glu	Glu	Lys	Leu	Ala	725	730	735	
His	Leu	Pro	Leu	Ala	Lys	Thr	Val	Ser	Val	Glu	Glu	Leu	Leu	Gln	Tyr	740	745	750	
Val	Glu	Leu	Gln	Asp	Pro	Val	Thr	Arg	Thr	Gln	Leu	Arg	Ala	Met	Ala	755	760	765	
Ala	Lys	Thr	Val	Cys	Pro	Pro	His	Lys	Val	Glu	Leu	Glu	Ala	Leu	Leu	770	775	780	
Glu	Lys	Gln	Ala	Tyr	Lys	Glu	Gln	Val	Leu	Ala	Lys	Arg	Leu	Thr	Met	785	790	795	800
Leu	Glu	Leu	Leu	Glu	Lys	Tyr	Pro	Ala	Cys	Glu	Met	Lys	Phe	Ser	Glu	805	810	815	
Phe	Ile	Ala	Leu	Leu	Pro	Ser	Ile	Arg	Pro	Arg	Tyr	Tyr	Ser	Ile	Ser	820	825	830	
Ser	Ser	Pro	Arg	Val	Asp	Glu	Lys	Gln	Ala	Ser	Ile	Thr	Val	Ser	Val	835	840	845	
Val	Ser	Gly	Glu	Ala	Trp	Ser	Gly	Tyr	Gly	Glu	Tyr	Lys	Gly	Ile	Ala	850	855	860	

34

Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe
 865 870 875 880
 Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr
 885 890 895
 Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly
 900 905 910
 Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly
 915 920 925
 Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu
 930 935 940
 Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu
 945 950 955 960
 His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln
 965 970 975
 His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln
 980 985 990
 Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala
 995 1000 1005
 Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val Ser
 1010 1015 1020
 Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly Arg
 1025 1030 1035 1040
 Tyr Ala Lys Asp Val Trp Ala Gly
 1045

<210> 3

<211> 30

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: PCR primer

<400> 3

gcaggagacg gggtggnnac aagctggacg

30

<210> 4

<211> 30

<212> DNA

<213> Synthetic sequence

35

<220>

<223> Description of the synthetic sequence: PCR primer

<400> 4

cgtccagctt gttnncaacc cgtctcctgc

30

<210> 5

<211> 34

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: PCR primer

<400> 5

gaagcaatga acaagnnnca gcgagcaaatt ccag

34

<210> 6

<211> 30

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: PCR primer

<400> 6

ctggatttgc tcgctgnnnc ttgttcattg

30

<210> 7

<211> 41

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: PCR primer

<400> 7

gctttgataa aaacttaaag tcaannnctt aaatttgtag g

41

<210> 8

<211> 40

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: PCR primer

<400> 8

cgtacaaatt taagnnnttg acttaagttt ttatcaaagc

40

36

<210> 9

<211> 1049

<212> PRT

<213> Bacillus megaterium

<400> 9

Met Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys
 1 5 10 15

Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys
 20 25 30

Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg
 35 40 45

Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp
 50 55 60

Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg
 65 70 75 80

Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn
 85 90 95

Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala
 100 105 110

Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val
 115 120 125

Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu
 130 135 140

Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn
 145 150 155 160

Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr
 165 170 175

Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala
 180 185 190

Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu
 195 200 205

Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg
 210 215 220

Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn
 225 230 235 240

37

Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg
 245 250 255

Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly
 260 265 270

Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu
 275 280 285

Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro
 290 295 300

Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn
 305 310 315 320

Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala
 325 330 335

Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp
 340 345 350

Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp
 355 360 365

Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser
 370 375 380

Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala
 385 390 395 400

Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly
 405 410 415

Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu
 420 425 430

Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys
 435 440 445

Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr
 450 455 460

Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn
 465 470 475 480

Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly
 485 490 495

Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro
 500 505 510

38

Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly
515 520 525

Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn
530 535 540

Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val
545 550 555 560

Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala
565 570 575

Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala
580 585 590

Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp
595 600 605

Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp
610 615 620

Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys
625 630 635 640

Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu
645 650 655

Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu
660 665 670

Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu
675 680 685

Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile
690 695 700

Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly
705 710 715 720

Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu
725 730 735

Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln
740 745 750

Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met
755 760 765

Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu
770 775 780

39

Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr
 785 790 795 800
 Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser
 805 810 815
 Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile
 820 825 830
 Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser
 835 840 845
 Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile
 850 855 860
 Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys
 865 870 875 880
 Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu
 885 890 895
 Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg
 900 905 910
 Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu
 915 920 925
 Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr
 930 935 940
 Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr
 945 950 955 960
 Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val
 965 970 975
 Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp
 980 985 990
 Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro
 995 1000 1005
 Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val
 1010 1015 1020
 Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly
 1025 1030 1035 1040
 Arg Tyr Ala Lys Asp Val Trp Ala Gly
 1045